



# SEQUENCE LISTING

<110> Houghans, Richard P.

<120> Chimeric Effector Cell Receptors Against Carcinoembryonic Antigen

<130> 002

<140> 10/006,771

<141> 2001-12-10

<150> 60/250,090

<151> 2000-11-30

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 7654

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2428)..(3759)

<223> Chimeric IgTCR sequence contained in retroviral vector. Retroviral vector sequence (non-coding regions) are incidental to the invention. The translated (coding region) is relevant to the invention. (pertinent to Figure 3.)

<400> 1

```
aagcttgcac gacctgcaggt cgactctagg cacataaaga aaaacataac taaccaagct      60
gcagccgaga cagtgaaaag aaccgttaaa acggtttgtt ttaaataaac tgaattattt      120
agagtcattt ctttggtagg aaagtacatt ggcacgtaaa ggagcccaaa gcaatctgtg      180
gaaagcccag gctgggagcc cagcagtttg catcccctcc tggcgtgtac ctaagggttt      240
cttaattgtg tggtttctaa atcttccaga gggtttgtct cattcacttc cacttcggtg      300
cacaatactt ggacgcggat ttactgtctt agcatctatc ggtggccctt cgattgaggc      360
tgaacctgag gccacttctt tcagcttggt aaggagagca caagcaccag aagaggctga      420
cccggcagac ctgtgggcat ttttaacaag ggcctcctgg gtctgtggga ggcaggctta      480
cataagggtgc aaattagaaa tataaataat aagcccatat caatttgtca tcttttttta      540
agctcaagtt ttgaaagacc ccacctgtag gtttggcaag ctagcttaag taacgccatt      600
ttgcaaggca tggaaaatac ataactgaga atagagaagt tcagatcaag gttaggaaca      660
gagagacagc agaatatggg ccaaacagga tatctgtggt aagcagttcc tgccccgctc      720
```

agggccaaga acagttggaa caggagaata tgggccaac aggatatctg tggtaagcag	780
ttcctgcccc ggctcagggc caagaacaga tgggtcccag atgcgggtccc gccctcagca	840
gtttctagag aaccatcaga tgtttccagg gtgcccgaag gacctgaaat gaccctgtgc	900
cttatttgaa ctaaccaatc agttcgcttc tcgcttctgt tcgcgcgctt ctgctccccg	960
agctcaataa aagagcccac aaccctcac tcggcgcgcc agtcctccga tagactgcgt	1020
cgcccgggta cccgtattcc caataaagcc tcttgctgtt tgcacccgaa tcgtggactc	1080
gctgatcctt gggaggggtct cctcagattg attgactgcc cacctcgggg gtctttcatt	1140
tggaggttcc accgagattt ggagaccct gccagggac caccgacccc ccgcccggga	1200
ggtaagctgg ccagcaactt atctgtgtct gtccgattgt ctagtgtcta tgactgattt	1260
tatgcgcctg cgtcggtact agttagctaa ctagctctgt atctggcgga cccgtgggtg	1320
aactgacgag ttcggaacac ccggccgcaa ccctgggaga cgtcccaggg acttcggggg	1380
ccgtttttgt ggcccgacct gagtcctaaa atcccgatcg tttaggactc tttggtgcac	1440
cccccttaga ggagggatat gtggttctgg taggagacga gaacctaaaa cagttcccgc	1500
ctccgtctga atttttgctt tcggtttggg accgaagccg cgccgcgcgt cttgtctgct	1560
gcagcatcgt tctgtgttgt ctctgtctga ctgtgtttct gtatttgtct gaaaatatgg	1620
gccccgggcta gactgttacc actcccttaa gtttgacctt aggtcactgg aaagatgtcg	1680
agcggatcgc tcacaaccag tcggtagatg tcaagaagag acgttgggtt accttctgct	1740
ctgcagaatg gccaaccttt aacgtcggat ggccgcgaga cggcaccttt aaccgagacc	1800
tcatcaccca ggttaagatc aaggtctttt cacctggccc gcatggacac ccagaccagg	1860
tcccctacat cgtgacctgg gaagccttgg cttttgacct ccctccctgg gtcaagccct	1920
ttgtacaccc taagcctccg cctcctcttc ctccatccgc cccgtctctc ccccttgaac	1980
ctcctcgttc gacccgcct cgatcctccc tttatccagc cctcactcct tctctaggcg	2040
cccccatatg gccatattgag atcttatatg gggcaccccc gcccttgta aacttcctg	2100
accctgacat gacaagagtt actaacagcc cctctctcca agctcactta caggcttcta	2160
cttagtccag cacgaagtct ggagacctct ggcggcagcc taccaagaac aactggaccg	2220
accggtggta cctcaccctt accgagtcgg cgacacagtg tgggtccgcc gacaccagac	2280
taagaaccta gaacctcgct ggaaaggacc ttacacagtc ctgctgacca cccccaccgc	2340
cctcaaagta gacggcatcg cagcttgat acacgccgcc cacgtgaagg ctgccgacct	2400
cgggggtgga ccatcctcta gactgcc atg gga tgg agc tgt atc atc ctc ttc	2454

Met Gly Trp Ser Cys Ile Ile Leu Phe																
1								5								
ttg gta gca aca gct aca ggt gtc cac tcc gac atc cag ctg acc cag	2502															
Leu Val Ala Thr Ala Thr Gly Val His Ser Asp Ile Gln Leu Thr Gln																
10 15 20 25																
agc cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc	2550															
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr																
30 35 40																
tgt aag gcc agt cag gat gtg ggt act tct gta gct tgg tac cag cag	2598															
Cys Lys Ala Ser Gln Asp Val Gly Thr Ser Val Ala Trp Tyr Gln Gln																
45 50 55																
aag cca ggt aag gct cca aag ctg ctg atc tac tgg aca tcc acc cgg	2646															
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg																
60 65 70																
cac act ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac	2694															
His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp																
75 80 85																
ttc acc ttc acc atc agc agc ctc cag cca gag gac atc gcc acc tac	2742															
Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr																
90 95 100 105																
tac tgc cag caa tat agc ctc tat cgg tcg ttc ggc caa ggg acc aag	2790															
Tyr Cys Gln Gln Tyr Ser Leu Tyr Arg Ser Phe Gly Gln Gly Thr Lys																
110 115 120																
gtg gaa atc aaa cga ggt ggc tca gga tcg ggt gga tcc ggc tct ggt	2838															
Val Glu Ile Lys Arg Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly																
125 130 135																
ggc tca gga tcg gag gtc caa ctg gtg gag agc ggt gga ggt gtt gtg	2886															
Gly Ser Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val																
140 145 150																
caa cct ggc cgg tcc ctg cgc ctg tcc tgc tcc gca tct ggc ttc gat	2934															
Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp																
155 160 165																
ttc acc aca tat tgg atg agt tgg gtg aga cag gca cct gga aaa ggt	2982															
Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly																
170 175 180 185																
ctt gag tgg att gga gaa att cat cca gat agc agt acg att aac tat	3030															
Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn Tyr																
190 195 200																
gcg ccg tct cta aag gat aga ttt aca ata tcg cga gac aac gcc aag	3078															
Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys																
205 210 215																
aac aca ttg ttc ctg caa atg gac agc ctg aga ccc gaa gac acc ggg	3126															
Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly																

220	225	230	
gtc tat ttt tgt gca agc ctt tac ttc ggc ttc ccc tgg ttt gct tat			3174
Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala Tyr	235	240 245	
tgg ggc caa ggg acc ccg gtc acc gtc tcc agt gct aag ccc acc acg			3222
Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Lys Pro Thr Thr	250 255	260 265	
acg cca gcg ccg cga cca cca aca ccg gcg ccc acc atc gcg tcg cag			3270
Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln	270 275	280	
ccc ctg tcc ctg cgc cca gag gcg gct cgg cca gcg gcg ggg ggc gca			3318
Pro Leu Ser Leu Arg Pro Glu Ala Ala Arg Pro Ala Ala Gly Gly Ala	285 290	295	
gtg cac acg agg ggg ctg gac ttc gcc ctg gat ccc aaa ctc tgc tac			3366
Val His Thr Arg Gly Leu Asp Phe Ala Leu Asp Pro Lys Leu Cys Tyr	300 305	310	
ctg ctg gat gga atc ctc ttc atc tat ggt gtc att ctc act gcc ttg			3414
Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu	315 320	325	
ttc ctg aga gtg aag ttc agc agg agc gca gag ccc ccc gcg tac cag			3462
Phe Leu Arg Val Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln	330 335	340 345	
cag ggc cag aac cag ctc tat aac gag ctc aat cta gga cga aga gag			3510
Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu	350 355	360	
gag tac gat gtt ttg gac aag aga cgt ggc cgg gac cct gag atg ggg			3558
Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly	365 370	375	
gga aag ccg aga agg aag aac cct cag gaa ggc ctg tac aat gaa ctg			3606
Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu	380 385	390	
cag aaa gat aag atg gcg gag gcc tac agt gag att ggg atg aaa ggc			3654
Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly	395 400	405	
gag cgc cgg agg ggc aag ggg cac gat ggc ctt tac cag ggt ctc agt			3702
Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser	410 415	420 425	
aca gcc acc aag gac acc tac gac gcc ctt cac atg cag gcc ctg ccc			3750
Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro	430 435	440	
cct cgc taa ctcgacgcgg ccgcggatcc ggattagtcc aatttggttaa			3799
Pro Arg			



agacaggata tcagtgggtcc aggctctagt ttgactcaa caatatcacc agctgaagcc	3859
tatagagtac gagccataga taaaataaaa gattttattht agtctccaga aaaagggggg	3919
aatgaaagac cccacctgta ggthttggcaa gctagcttaa gtaacgccat ttgcaaggc	3979
atggaaaata cataactgag aatagagaag ttcagatcaa ggtaggaac agagagacag	4039
cagaatatgg gccaaacagg atatctgtgg taagcagttc ctgccccgct cagggccaag	4099
aacagttgga acaggagaat atggggccaaa caggatatct gtggtaaagca gttcctgccc	4159
cggctcaggg ccaagaacag atgggtcccca gatgcgggtcc cgccctcagc agthttctaga	4219
gaaccatcag atgthttccag ggtgccccaa ggacctgaaa tgacctgtg cthttatthga	4279
actaaccaat cagthtcgctt ctcgcttctg ttcgcgcgct tctgctcccc gagctcaata	4339
aaagagccca caaccctca ctcggcgcgc cagtcctccg atagactgcg tgcgccgggt	4399
acctgtgttc tcaataaacc ctcttgcaagt tgcataccgac tctgtgtctc gctgttcctt	4459
gggaggggtct ctctgagtga ttgactaccc gtcagcgggg tctthtcagtt tctccacct	4519
acacagggtct cactaacatt cctgatgtgc cgcagggaact ccgtcagccc ggtthttgtt	4579
tataataaaa tgcaagaaca gtgttccctt caagccagac tacatcctga ctctcggctt	4639
tataaaagaa tgthgaaggg ctctgtggac tatctgccac acgactthtt aagatthtta	4699
tgccctctgg atgagggatt tagtcaatct atcctcgtct atthttgctgg ctctccgta	4759
thttaaatth ctagthttga ctcccttctt gagagcacgg cgattgcaga gtagthtaata	4819
ctctgagggc aggtctctgt gaaaaggtht cctgggctca gtgtgagatt ttgccataaa	4879
aaggggtcct gccctgtgt acagacagat cggaatctag agtgcatact cagagtcccc	4939
gcggttccgg ggctctgatc tcagggcata tthgcctaga gatcctctac gccggacgca	4999
tcgtggccgg gtaccgagct cgaattcgta atcatggtca tagctgtthc ctgtgtgaaa	5059
ttgttatccg ctcaaatth cacacaacat acgagccgga agcataaagt gtaaagcctg	5119
gggtgcctaa tgagtgaact aactcacatt aattgcgtht cgctcactgc ccgctthcca	5179
gtcgggaaac ctgtcgtgcc agctgcatta atgaatcggc caacgcgcgg ggagaggcgg	5239
thttgcgtatt gggcgctctt ccgcttctc gctcactgac tgcgtgcgct cggctgttcg	5299
gctgcggcga gcggtatcag ctcaactcaa ggcggttaata cggthtatcca cagaatcagg	5359
ggataacgca ggaaagaaca tgtgagcaaa aggccagcaa aaggccagga accgtaaaaa	5419
ggccgcgtht ctggcgthtt tccataggct ccgccccct gacgagcatc acaaaaatcg	5479

acgctcaagt cagaggtggc gaaacccgac aggactataa agataccagg cgtttcccc	5539
tggaagctcc ctctgctgct ctctgtttcc gaccctgccg cttaccggat acctgtccgc	5599
ctttctccct tcgggaagcg tggcgctttc tcatagctca cgctgtaggt atctcagttc	5659
ggtgtaggtc gtctgctcca agctgggctg tgtgcacgaa cccccgttc agcccgaccg	5719
ctgcgcctta tccggtaact atcgtcttga gtccaacccg gtaagacacg acttatcgcc	5779
actggcagca gccactggta acaggattag cagagcgagg tatgtaggcg gtgctacaga	5839
gttcttgaag tgggtggccta actacggcta cactagaagg acagtatttg gtatctgcgc	5899
tctgctgaag ccagttacct tcggaaaaag agttggtagc tcttgatccg gcaaacaac	5959
caccgctggt agcgggtggt tttttgtttg caagcagcag attacgcgca gaaaaaagg	6019
atctcaagaa gatcctttga tcttttctac ggggtctgac gctcagtgga acgaaaactc	6079
acgttaaggg attttggta tgagattatc aaaaaggatc ttcacctaga tccttttaa	6139
ttaaaaatga agttttaaat caatctaaag tatatatgag taaacttggc ctgacagtta	6199
ccaatgctta atcagtgagg cacctatctc agcgatctgt ctatttcgtt catccatagt	6259
tgctgactc cccgtcgtgt agataactac gatacgggag ggcttaccat ctggccccag	6319
tgctgcaatg ataccgcgag acccacgctc accggctcca gatttatcag caataaacca	6379
gccagccgga agggccgagc gcagaagtgg tcctgcaact ttatccgcct ccatccagtc	6439
tattaattgt tgccgggaag ctagagtaag tagttcgcca gttaatagtt tgcgcaacgt	6499
tgttgccatt gctacaggct cgtgggtgtc cgctcgtcgt ttggtatggc ttcattcagc	6559
tccggttccc aacgatcaag gcgagttaca tgatccccca tgttgtgcaa aaaagcggtt	6619
agtccttcg gtctccgat cgttgctcaga agtaagttgg ccgcagtgtt atcactcatg	6679
gttatggcag cactgcataa ttctcttact gtcatgcat ccgtaagatg cttttctgtg	6739
actggtgagt actcaaccaa gtcattctga gaatagtgtg tgcggcgacc gagttgctct	6799
tgcccgcgct caatacggga taataccgcg ccacatagca gaactttaaa agtgctcatc	6859
attggaaaac gttcttcggg gcgaaaactc tcaaggatct taccgctgtt gagatccagt	6919
tcgatgtaac ccactcgtgc acccaactga tcttcagcat cttttacttt caccagcgtt	6979
tctgggtgag caaaaacagg aaggcaaaat gccgcaaaaa agggaataag ggcgacacgg	7039
aaatgttgaa tactcatact cttccttttt caatattatt gaagcattta tcagggttat	7099
tgtctcatga gcggatacat atttgaatgt atttagaaaa ataaacaaat aggggttccg	7159
cgcacatttc cccgaaaagt gccacctgac gtctaagaaa ccattattat catgacatta	7219

acctataaaa ataggcgtat cacgaggccc tttcgtctcg cgcgtttcgg tgatgacggt 7279  
gaaaacctct gacacatgca gctcccgag acggtcacag cttgtctgta agcggatgcc 7339  
gggagcagac aagcccgta gggcgctca gcgggtgttg gcgggtgtcg gggctggctt 7399  
aactatgcgg catcagagca gattgtactg agagtgcacc atatgcggtg tgaaataccg 7459  
cacagatgcg taaggagaaa ataccgcac aggcgccatt cgccattcag gctgcgcaac 7519  
tgttgggaag ggcgatcggg gcgggcctct tcgctattac gccagctggc gaaaggggga 7579  
tgtgctgcaa ggcgattaag ttgggtaacg ccagggtttt cccagtcacg acgttgtaaa 7639  
acgacggcca gtgcc 7654

<210> 2  
<211> 443  
<212> PRT  
<213> Homo sapiens

<400> 2

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15

Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala  
20 25 30

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val  
35 40 45

Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
50 55 60

Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg  
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
85 90 95

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu  
100 105 110

Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly  
115 120 125



Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Glu Val Gln  
130 135 140

Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg  
145 150 155 160

Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser  
165 170 175

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile  
180 185 190

His Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg  
195 200 205

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Phe Leu Gln Met  
210 215 220

Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu  
225 230 235 240

Tyr Phe Gly Phe Pro Trp Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val  
245 250 255

Thr Val Ser Ser Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro  
260 265 270

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu  
275 280 285

Ala Ala Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp  
290 295 300

Phe Ala Leu Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe  
305 310 315 320

Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe Ser  
325 330 335

Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr  
340 345 350

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys

355

360

365

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn  
 370 375 380

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu  
 385 390 395 400

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly  
 405 410 415

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr  
 420 425 430

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg  
 435 440

&lt;210&gt; 3

&lt;211&gt; 422

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens and Mus sp.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (8)..(421)

<223> hMn14 VH, humanized (CDR-grafted) anti-CEA antibody heavy chain V  
 region (aa20-138) with leader (aal-19) (pertinent to Fig. 4A.)

&lt;400&gt; 3

cctcacc atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct 49  
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala  
 1 5 10

aca ggt gtc cac tcc gag gtc caa ctg gtg gag agc ggt gga ggt gtt 97  
 Thr Gly Val His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val  
 15 20 25 30

gtg caa cct ggc cgg tcc ctg cgc ctg tcc tgc tcc gca tct ggc ttc 145  
 Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe  
 35 40 45

gat ttc acc aca tat tgg atg agt tgg gtg aga cag gca cct gga aaa 193  
 Asp Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys  
 50 55 60

ggt ctt gag tgg att gga gaa att cat cca gat agc agt acg att aac 241  
 Gly Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn  
 65 70 75

tat gcg ccg tct cta aag gat aga ttt aca ata tcg cga gac aac gcc 289

Tyr Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala  
 80 85 90

aag aac aca ttg ttc ctg caa atg gac agc ctg aga ccc gaa gac acc 337  
 Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr  
 95 100 105 110

ggg gtc tat ttt tgt gca agc ctt tac ttc ggc ttc ccc tgg ttt gct 385  
 Gly Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala  
 115 120 125

tat tgg ggc caa ggg acc ccg gtc acc gtc tcc tca g 422  
 Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser  
 130 135

<210> 4

<211> 138

<212> PRT

<213> Homo sapiens and Mus sp.

<400> 4

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
 1 5 10 15

Val His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln  
 20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe  
 35 40 45

Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60

Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn Tyr Ala  
 65 70 75 80

Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn  
 85 90 95

Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val  
 100 105 110

Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala Tyr Trp  
 115 120 125

Gly Gln Gly Thr Pro Val Thr Val Ser Ser  
 130 135

<210> 5  
<211> 712  
<212> DNA  
<213> Homo sapiens and Mus sp.

<220>  
<221> CDS  
<222> (14)..(712)  
<223> hMN14 VLCK, humanized (CDR-grafted) anti-CEA antibody kappa light chain V region (aa20-126), with human constant CK domain (aa127-232) and leader (aa1-19). (pertinent to Figure 4B.)

<400> 5  
tctagacctc acc atg gga tgg agc tgt atc atc ctc ttc ttg gta gca 49  
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala  
1 5 10  
  
aca gct aca ggt gtc cac tcc gac atc cag ctg acc cag agc cca agc 97  
Thr Ala Thr Gly Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser  
15 20 25  
  
agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt aag gcc 145  
Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala  
30 35 40  
  
agt cag gat gtg ggt act tct gta gct tgg tac cag cag aag cca ggt 193  
Ser Gln Asp Val Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly  
45 50 55 60  
  
aag gct cca aag ctg ctg atc tac tgg aca tcc acc cgg cac act ggt 241  
Lys Ala Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly  
65 70 75  
  
gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc acc ttc 289  
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe  
80 85 90  
  
acc atc agc agc ctc cag cca gag gac atc gcc acc tac tac tgc cag 337  
Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln  
95 100 105  
  
caa tat agc ctc tat cgg tgc ttc ggc caa ggg acc aag gtg gaa atc 385  
Gln Tyr Ser Leu Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile  
110 115 120  
  
aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat 433  
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
125 130 135 140  
  
gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac 481  
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
145 150 155  
  
ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc 529

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
160 165 170

caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac 577  
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
175 180 185

agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac 625  
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
190 195 200

gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc 673  
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
205 210 215 220

tcg ccc gtc aca aag agc ttc aac agg gga gag tgt taa 712  
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
225 230

<210> 6  
<211> 232  
<212> PRT  
<213> Homo sapiens and Mus sp.

<400> 6

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15

Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala  
20 25 30

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val  
35 40 45

Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
50 55 60

Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg  
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
85 90 95

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu  
100 105 110

Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val  
115 120 125

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys  
130 135 140

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
145 150 155 160

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn  
165 170 175

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
180 185 190

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
195 200 205

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
210 215 220

Lys Ser Phe Asn Arg Gly Glu Cys  
225 230